Amendments to the Claims

This listing of claims will replace all prior versions, and listings of claims in the application:

Listing of Claims:

1. (Currently Amended) A method for minimizing the aggregation tendencies of ~~an amyloid forming protein~~ human kappa-IV immunoglobulin light chain, the method comprising:

a) identifying SMA or LEN mutation in the amino acid sequence of ~~said protein~~ the light chain that leads to fibril formation;

b) substituting each mutation into SMA or LEN to identify the residues of a peptide that contribute to fibril formation;

c) synthesizing peptides spanning most of the light chain variable region that interacts with an endoplasmic reticulum chaperone selected from the group consisting of BiP, Hsp 70, and combinations thereof;

d) determining the V_L-derived peptides for their ability to prevent fibril formation in vitro wherein the peptides are selected from the group consisting of TDFTLTI (SEQ ID NO: 5), FTLTISS (SEQ ID NO: 1), FTLKISR (SEQ ID NO: 6), FTLEISR (SEQ ID NO: 12), LTLKLSR (SEQ ID NO: 13) and combinations thereof; and

e) ~~preventing~~ inhibiting fibril formation by inserting the said peptide into the complimentary region of the light chain variable domain.

2. (Previously Amended) The method as recited in claim 1 wherein the method is conducted in a cell.

3. (Canceled)

4. (Canceled)

5. (Currently Amended) The method as recited in claim ~~3~~ 1 wherein the peptide is inserted between residue position numbers 60 and 83 of the human kappa-IV light chain.

6. (Canceled)

7. (Previously Amended) The method as recited in claim 1 wherein the peptide is inserted when the ~~amyloid forming~~ protein is partially unfolded.

8. (Canceled)

9. (Canceled)

10. (Currently Amended) The method as recited in claim ~~9~~ 7 wherein the peptide is inserted at a hairpin anchorage point in the human kappa-IV protein and its derivatives selected from the group consisting of TDFTLTI (SEQ ID NO: 5), FTLTISS (SEQ ID NO: 1), FTLKISR (SEQ ID NO: 6), FTLEISR (SEQ ID NO: 12), LTLKLSR (SEQ ID NO: 13), and combinations thereof.

11-13 (Canceled)

14. (Original) A peptide for insertion in an intact human kappa-IV light chain variable domain, the peptide comprising the following amino acid sequence:

Phe_{71}-Thr_{72}-Leu_{73}-Thr_{74}-Ile_{75}-Ser_{76}-Ser_{77}

wherein the subscript numbers are the residue location points in the domain.

15. (Currently Amended) A method for ~~preventing~~ minimizing amyloid formation in human kappa-IV light chain variable domain, the method comprising inserting the peptide Phe_{71}-Thr_{72}-Leu_{73}-Thr_{74}-Ile_{75}-Ser_{76}-Ser_{77} into the domain, wherein the subscript numbers indicate the residue location on the domain.

16. (Original) The method as recited in claim 15 wherein the domain is partially unfolded at the time of insertion.

17-22. (Canceled)

23. (New) A method for minimizing the aggregation tendencies of an amyloid forming protein, the method comprising:

a) identifying submotifs in primary structures of the protein that induce fibril formation; and

b) interacting a biological molecule inhibitor with said critical submotifs so as to stabilize the normal conformation of the protein.

24. (New) The method as recited in claim 23 wherein the step of identifying submotifs comprises mutating the amino acid sequence of said protein.

25. (New) The method as recited in claim 23 wherein the protein is human kappa-IV light chain variable domain or a greek key fold protein selected from the group consisting of antibody constant domains, transthyretin, beta-2 microglobulin, serine protease inhibitors, and crystalline.

26. (New) The method as recited in claim 25 wherein the inhibitor interacts with the human kappa-IV light chain between residue position numbers 60 and 83 of

the light chain.

27. (New) The method as recited in claim 26 wherein the inhibitor is a peptide having the amino acid sequence Phe_{71}-Thr_{72}-Leu_{73}-Thr_{74}-Ile_{75}-Ser_{76}-Ser_{77} (SEQ. ID No: 1) and wherein the subscripts denote the positions of the amino acids in the residue.

28. (New) The method as recited in claim 23 wherein the inhibitor is inserted when the amyloid forming protein is partially unfolded.

29. (New) The method as recited in claim 23 wherein the inhibitor is serine protease.

30. (New) A method for preventing fibril assembly of human kappa-IV immunoglobulin, the method comprising:

a) identifying the residues of the peptide that contribute to fibril formation by mutating the amino acid sequence of human kappa-IV immunoglobulin; and

b) blocking said fibril formation by inserting biological molecules into the amino acid sequence.

31. (New) The method as recited in claim 30 wherein the biological molecules are peptides selected from the group consisting of TDFTLTI (SEQ ID NO: 5), FTLTISS (SEQ ID NO: 1), FTLKISR (SEQ ID NO: 6), FTLEISR (SEQ ID NO: 12), LTLKLSR (SEQ ID NO: 13), and combinations thereof.

32. (New) A method for minimizing the aggregation tendencies of human kappa-IV immunoglobulin light chain protein in a cell, the method comprising:

a) expressing the protein in a cell;

b) identifying the residues of a peptide that contribute to fibril formation by

mutating the amino acid sequence of the protein; and

c) interacting the peptide with the cell to inhibit fibril formation.

33. (New) The method as recited in claim 32 wherein the peptide is TDFTLTI (SEQ ID NO: 5), or FTLTISS (SEQ ID NO: 1), or FTLKISR (SEQ ID NO: 6), or FTLEISR (SEQ ID NO: 12), or LTLKLSR (SEQ ID NO: 13).

34. (New) The method as recited in claim 32 wherein the peptide contains an amino acid sequence which is also contained in the protein.